



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/644,582	08/20/2003	D. Navin Chandra	GEN-001	5207
51414 7590 09/18/2008 GOODWIN PROCTER LLP PATENT ADMINISTRATOR EXCHANGE PLACE BOSTON, MA 02109-2881				
EXAMINER PHAM, KHANH B				
ART UNIT 2166		PAPER NUMBER		
NOTIFICATION DATE 09/18/2008		DELIVERY MODE ELECTRONIC		

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

PatentBos@goodwinprocter.com
hmcpeake@goodwinprocter.com
glenn.williams@goodwinprocter.com



UNITED STATES PATENT AND TRADEMARK OFFICE

Commissioner for Patents
United States Patent and Trademark Office
P.O. Box 1450
Alexandria, VA 22313-1450
www.uspto.gov

**BEFORE THE BOARD OF PATENT APPEALS
AND INTERFERENCES**

Application Number: 10/644,582
Filing Date: August 20, 2003
Appellant(s): CHANDRA ET AL.

Joel E. Lehrer
For Appellant

EXAMINER'S ANSWER

This is in response to the appeal brief filed 6/27/2008 appealing from the Office action mailed 1/18/2008.

(1) Real Party in Interest

A statement identifying by name the real party in interest is contained in the brief.

(2) Related Appeals and Interferences

The examiner is not aware of any related appeals, interferences, or judicial proceedings which will directly affect or be directly affected by or have a bearing on the Board's decision in the pending appeal.

(3) Status of Claims

The statement of the status of claims contained in the brief is correct.

The amendment after final rejection filed concurrently with the Appeal Brief on 6/17/2008 has been entered.

(5) Summary of Claimed Subject Matter

The summary of claimed subject matter contained in the brief is correct.

(6) Grounds of Rejection to be Reviewed on Appeal

The appellant's statement of the grounds of rejection to be reviewed on appeal is correct.

(7) Claims Appendix

The copy of the appealed claims contained in the Appendix to the brief is correct.

(8) Evidence Relied Upon

2002/0087275 A1	KIM	7-2002
2002/0198858 A1	STANLEY ET AL.	12-2002

(9) Grounds of Rejection

The following ground(s) of rejection are applicable to the appealed claims:

Claim Rejections - 35 USC § 102

1. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

2. **Claims 26-39 92-95, 97-106 are rejected** under 35 U.S.C. 102(e) as being anticipated by Kim et al. (US2002/0087275 A1), hereinafter "Kim".

As per claim 26, Kim teaches a computer system for storing life science information comprising:

- "an electronic database storage module for storing a library of case frames, each case frame comprising: at least two unspecified object identifiers; and a relationship connector, wherein the relationship connector relates two of the at least two object identifiers to each other based on a causal relationship between the object identifier and is based on a life science ontology" at [0046]-[0047], [0055], [0057] and Fig. 1;

- “an inference engine module for managing the addition of new data to a database of life science data by translating the new data into a form compatible with the database” at [0041], [0073]-[0074], [0093];
- “selecting one of the case frame as a template to represent the new data based at least in part on the life science ontology” at [0073] and Tables 1-3;
- “and for assigning elements of the new data to the object identifiers and relationship connectors, thus assuring the newly created life science assertions conform to the life science ontology at [0081]-[0098].

As per claim 27, Kim teaches the system of claim 26, wherein “a set of said case frames define a biological function” at [0112].

As per claim 28, Kim teaches the system of claim 27, wherein “the biological function comprises a chemical reaction” at [0124].

As per claim 29, Kim teaches the system of claim 27, wherein “the biological function comprises transport” at [0124].

As per claim 30, Kim teaches the system of claim 27, wherein “the biological function comprises digestion of a biomolecule” at [0124].

As per claim 31, Kim teaches the system of claim 26, wherein “at least one of the at least two object identifiers identifies a biomolecule” at [0070].

As per claim 32, Kim teaches the system of claim 26, wherein “at least one of the at least two object identifiers identifies a biological function” at [0124].

As per claim 33, Kim teaches the system of claim 26, wherein “at least one of the at least two object identifiers identifies a relationship connector” at [0089]-[0091].

As per claim 34, Kim teaches the system of claim 26, wherein “the relationship connector represents an identity relationship” at [0091].

As per claim 35, Kim teaches the system of claim 26, wherein “the relationship connector represents a product relationship” at [0091].

As per claim 36, Kim teaches the system of claim 26, wherein “the relationship connector represents a substrate relationship” at [0103].

As per claim 37, Kim teaches the system of claim 26, wherein “the relationship connector represents an enzymatic relationship” at [0107].

As per claim 38, Kim teaches the system of claim 26 further comprising “a graphical user interface configured to permit a user to query the database based on the relationship connector” at Fig. 7.

As per claim 39, Kim teaches the system of claim 26 further comprising “a data input interface configured to accept user instructions relating to the creation of a new case frame” at Fig. 7.

As per claim 92, Kim teaches the system of claim 26, wherein “the inference engine further modifies the selected case frames such that the selected case frames more accurately represent the new data” at [0081]-[0087] and [0113]-[0120].

As per claim 93, Kim teaches the system of claim 92, wherein “the modifications comprise one or more of the addition of new fields, the addition of new relationships, and the addition of metadata” at [0074]-[0077].

As per claim 94, Kim teaches the system of claim 93, wherein “the metadata comprises one or more of the source of the new data, the data the new data was received, the time the new data was received, and the experimental conditions under which the new data was created” at [0077].

As per claim 95, Kim teaches the system of claim 26, further comprising: “a harmonization and transfer module for interfacing with multiple disparate sources of life science data and receiving the new data” at [0346] and Figs. 6, 13.

As per claim 97, Kim teaches the system of claim 95, wherein “the harmonization and transfer module further translates the received data into a data format compatible with the case frames” at Fig. 13.

As per claim 98, Kim teaches the system of claim 26, further comprising “a discovery environment for displaying a pathways among the plurality of case frames, the pathways representing causal relationship among the case frames” at Figs. 2-5.

As per claim 101, Kim teaches a system for storing life science data comprising:

- “an electronic database for storing a plurality of case frames, each case frame comprising at least two object identifiers; and a relationship connector, wherein the relationship connector relates two of the at least two object identifiers to each other and is based on a life science ontology” at [0046]-[0047], [0055] and Fig. 1
- “wherein the database comprises case frames representing at least enzyme reactions, binding interactions, modifications of polymers, protein phosphorylation reactions, gene expressions, acetylation, peptide-bon cleavage, glycosylation, lipidation, fatty-acylation, methylations, metallations, cross-linking, hydroxylation, sulfation, ADP-ribonsylation, translocation, and transcriptional activations” at [0041]-[0043] and [0124].

As per claim 102, Kim teaches the system of claim 101, wherein “the case frame representing protein phosphorylation reactions comprises a reactant, a product, and a catalyst” at [0102]-[0112].

As per claim 103, Kim teaches the system of claim 101, wherein the case frame representing gene expressions comprises a gene and a gene product” at [0124].

As per claim 104, Kim teaches the system of claim 101, wherein “the case frame representing transcriptional activation comprises a gene expression, an activation, and a transcriptional activator” at [0138]-[0145].

As per claim 105, Kim teaches the system of claim 101, further comprising “a harmonization and transfer module for interfacing with multiple disparate sources of life science data and receiving new data for inclusion in the database” at [0346] and Fig. 6.

As per claim 106, Kim teaches the system of claim 105, further comprising “an interference engine for managing the addition of the new data by instantiating a subset of the plurality of case frames to represent the new data and assuring the instantiated case frames conform to the life science ontology, thereby creating life science assertions in the database” at [0081]-[0087] and [0113]-[0120].

Claim Rejections - 35 USC § 103

3. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

4. **Claims 40, 96, 99-100 are rejected** under 35 U.S.C. 103(a) as being unpatentable over **Kim** as applied to claims 26-39 above, and in view of Stanley et al. (US 2002/0198858 A1), hereinafter “**Stanley**”.

As per claim 40, Askenazi teaches the system of claim 26 as discussed above. Kim does not explicitly teach “an access manager configured to restrict access of a user to one or more portions of the electronic database” as claimed. However, Stanley

teaches a biological database includes an access manger layer to restrict access of a user to one or more portions of the electronic database at Figs. 15-16. Thus, it would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine Stanley with Kim's teaching in order to enhance the security of the database and protect sensitive data in the database from unauthorized users.

As per claim 96, Kim teaches the system of claim 95 discussed above. Kim does not explicitly teach "the received data is received in XML format". However, Stanley teaches a biological database utilizing XML format at [0351]. Thus, it would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine Stanley with Kim's teaching to employ XML because XML is a well known data format, which often used as a common format for extracting data from plurality of different data sources.

As per claim 99, Kim teaches the system of claim 26 discussed above. Kim does not explicitly teach "a managed account interface for attributing access restrictions to one or more case frames in the database". However, Stanley teaches a biological database includes an access manger layer to restrict access of a user to one or more portions of the electronic database at Figs. 15-16. Thus, it would have been obvious to one of ordinary skill in the art at the time of the invention was made to combine Stanley with Kim's teaching in order to enhance the security of the database and protect sensitive data in the database from unauthorized users.

As per claim 100, Kim and Stanley teach the system of claim 99 discussed above. Stanley also teaches: "wherein the access restrictions comprise one or more public access rights, subscription-based rights, and proprietary access rights" at Figs. 15-16.

10) Response to Argument

The inventions:

Appellant's invention is directed to an electronic database storage to store a library of case frames, wherein each case frame include at least two object identifiers and a relationship connector. For example, Appellant's Fig. 2 shows at least two object identifiers 206 and 210 and a line connecting two object identifiers represents a relationship connector. New data can be added to the database using one of the case frame as a template.

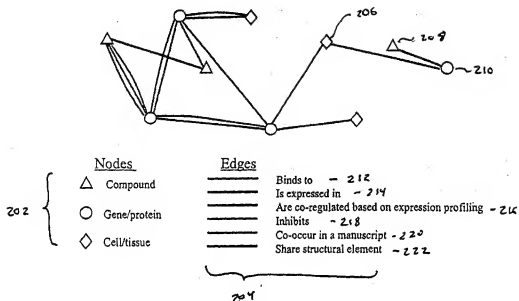
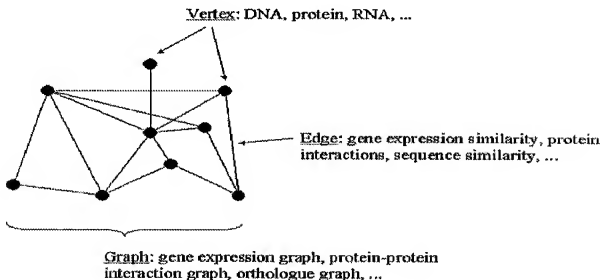


FIG. 2

Similarly, Kim teach a system and method for visualization and storing of biomolecular relationship using graph, as shown in Kim's Fig. 1:



Claim 26 is rejected under 35 U.S.C 102(e) as being anticipated by Kim

Appellant argued that Kim does not anticipate the invention of claim 26 because Kim does not teach the claimed "case frames" and "selection of case frame". The examiner respectfully disagrees and traverses appellant's arguments.

Response to Appellant's argument: A table is not a case frame

First, the component of a case frame is defined in claim 26 as follows:

...each case frame comprising:

- at least two unspecified object identifiers;
- a relationship connector, wherein the relationship connector relates two of the at least two object identifiers to each other based on a causal relationship between the object identifiers...

As seen in Kim's Fig. 1 above, Kim clearly teaches a plurality of case frames.

Kim also teaches a database for storing a library of case frames as [0047] as follows:

[0047] In some embodiments, the disclosed method can use and manipulate large databases, including object-oriented databases, for the storage and organization of molecular relational graph data (or gene-graph data), and can implement molecular relational graphing models for proteome and genome mapping data. A molecular relational graphing database can comprise large data sets from a variety of sources, such as gene expression analysis, proteome analysis, genome mapping, and functional genome annotation. Data objects, n-ary operations, and graph func-

Kim's paragraphs [0055] teaches that **"Vertices can be labeled with the identities of the biological molecules"**, which corresponds to the claimed "object identifiers" and Kim's paragraph [0057] teaches that **"By "edge" is it meant a**

connection between two vertices". Kim therefore clearly anticipated the claimed case frame. The detailed implementation of Kim's graph database can be found at paragraphs [0069]-[0098], and Tables 1-3, which shows that vertex's labels are stored in a table under "property_name" field.

Response to Appellant's arguments : No selection of Case Frames

Appellant argued that Kim fails to anticipate the claim because there is no mention that the Kim system "selects one of the case frames as a template to represent the new data". On the contrary, Kim teaches at least at paragraphs [0094]-[0098] the step to add new data representing the relationship of protein-protein interaction between Yeas Protein Molecules by selecting a case frame comprising a pair of vertices and a relationship connector and assigning elements of the new data to the object identifier (i.e. defining labels of the two vertices) and relationship connectors (i.e. edge direction and weight).

[0094] Illustration 4: Defining Edges Representing the Relationship of Protein-protein Interaction between Yeast Protein Molecules

[0095] Whole genome-scale study of protein-protein interactions has been carried out for yeast (Uetz et al. (2000)). Out of more than 6,000 proteins, 1,004 yeast proteins were reported to participate in 957 physical interactions with other protein molecules in yeast two-hybrid assays. In order to study large number of protein-protein interactions found in yeast cells, interactions between yeast protein molecules can be represented effectively using edges defined in molecular relational graphs. To define an edge representing a physical interaction between a pair of yeast proteins, vertices representing the two participating protein molecules can be defined first. Once the

vertices are defined, an edge can be defined by, for example, the following three components:

[0096] (1) Labels of input vertices and output vertices representing the involved protein molecules.

[0097] (2) A Boolean variable, DIRECTED, representing whether the edge is directed (thus respecting the input to output designation) or undirected. Since the protein-protein interactions are symmetrical relationships for this example, DIRECTED=FALSE.

[0098] (3) An edge weight table in which (property, value) pairs reflecting the properties of relationships are stored. In the simplest form, the table contains a list of (property, value) pairs such as: (assay_system, two hybrid), (assay_method, beta gal), and (strength, 1200).

Kim also teaches at [0101]-[0110] that a different case frame comprising a set of vertices and edges is selected to represent more complex data such as Metabolic Pathways in the Cell. Kim also teaches at [0087] that **"a vertex representing a yeast gene, GRX1, is created from a vertex representing an ORF, YCL035C, and a vertex representing a protein molecule, Grx1"**. Kim's system therefore allows using pre-defined case frame to represent new data.

In response to Appellant's argument that the references fail to show certain features of applicant's invention, it is noted that the features upon which applicant relies (i.e., "a library of pre-defined case frames that include both object type information and pre-defined connectors", "case frame go well beyond simple data structures described in Kim", "facilitates an automated and rapid expansion of the database", "invaluable aide in the drug development process") are not recited in the rejected claim(s). Although the claims are interpreted in light of the specification,

limitations from the specification are not read into the claims. See *In re Van Geuns*, 988 F.2d 1181, 26 USPQ2d 1057 (Fed. Cir. 1993).

Claims 101 is rejected under 35 U.S.C 102(e) as being anticipated by Kim

Regarding claim 101, Appellant argued that Kim does not teach "the database comprises case frames representing at least enzyme reactions, binding interactions, modifications of polymers, protein phosphorylation reactions, gene expressions, acetylation, peptide-bond cleavage, glycosylation, lipidation, fatty-acylation, methylation, metallation, cross-linking, hydroxylation, sulfation, ADP-ribosylation, translocation and transcriptional activations". On the contrary, Kim teaches this limitation at [0041]-[0043] and [0124]. For example, Kim's paragraph [0124] teaches a sample of possible types of molecular relational graph can be stored in the database:

[0123] Possible types of molecular relational graph include but are not limited to the following:

[0124] molecular relational graph representing physical mapping of genes, open reading frames, single nucleotide polymorphisms, expressed sequence tags, sequence tag sites, or a combination thereof; molecular relational graph representing genetic mapping of genes, open reading frames, single nucleotide polymorphisms, expressed sequence tags, sequence tag sites, or a combination thereof; molecular relational graph representing radiation-hybrid mapping of genes; molecular relational graph representing orthologous relationships between genes; molecular relational graph representing paralogous relationships between genes; molecular relational graph representing homologous relationships between genes; molecular relational graph representing structural relationships between proteins; molecular relational graph representing gene expression regulation; molecular relational graph representing gene translation regulation; molecular relational graph representing protein-protein interactions; molecular relational graph representing protein-

DNA interactions; molecular relational graph representing enzyme functions; molecular relational graph representing chemical metabolism; molecular relational graph representing cellular signal transduction pathways; and molecular relational graph representing functional gene annotation, functional pathways, functional groups, or a combination.

Claims 40, 96, 99 and 100 are rejected under 35 U.S.C 103(a) as being unpatentable over Kim in view of Stanley.

In view of the discussion above, the rejection of claims 40, 96, 99 and 100 are maintained.

(11) Related Proceeding(s) Appendix

No decision rendered by a court or the Board is identified by the examiner in the Related Appeals and Interferences section of this examiner's answer.

For the above reasons, it is believed that the rejections should be sustained.

Respectfully submitted,

/Khanh B. Pham/

Primary Examiner

AU 2166

Conferees:

/Hosain T Alam/

Supervisory Patent Examiner, Art Unit 2166

/Vincent F. Boccio/ VFB

Primary Examiner, Art Unit 2169

Appeal Specialist TC2100